

09865-06207

1	GGATAAGCCT	GGGGCCAGCA	TGAGCCAGAG	GGAGGGAAGT	CTGGAAGACG
	CCTATTTCGGA	CCCCGGTCGT	ACTCGGTCTC	CCTCCCTTCA	GACCTTCTGG
1		M	S Q R	E G S	L E D H
51	ACCAGACTGA	CTCCTCAATC	TCATTCTTAC	CCCATTGGA	GGCCAAGATC
	TGGTCTGACT	GAGGAGTTAG	AGTAAGGATG	GGGTAAACCT	CCGGTTCTAG
12	Q T D	S S I	S F L P	H L E	A K I
101	CGCCAGACAC	ACAACCTTGC	CCGCCTCCTG	ACCAAATATG	CAGAACAACT
	GCGGTCTGTG	TGTGGAACG	GGCGGAGGAC	TGGTTTATAC	GTCTTGTTGA
28	R Q T H	N L A	R L L	T K Y A	E Q L
151	TCTGGAGGAA	TACGTGCAGC	AACAGGGAGA	GCCCTTTGGG	CTGCCGGGCT
	AGACCTCCTT	ATGCACGTCG	TTGTCCCTCT	CGGGAAACCC	GACGGCCCCG
45	L E E	Y V Q Q	Q G E	P F G	L P G F
201	TCTCACCACC	GCGGCTGCCG	CTGGCCGGCC	TGAGTGGCCC	GGCTCCGAGC
	AGAGTGGTGG	CGCCGACGGC	GACCGGCCGG	ACTCACCGGG	CCGAGGCTCG
62	S P P	R L P	L A G L	S G P	A P S
251	CATGCAGGGC	TACCGGTGTC	CGAGCGGCTG	CGGCAGGATG	CAGCCGCCCT
	GTACGTCCCG	ATGGCCACAG	GCTCGCCGAC	GCCGTCCTAC	GTCGGCGGGA
78	H A G L	P V S	E R L	R Q D A	A A L
301	GAGTGTGCTG	CCGCGCTGT	TGGATGCCGT	CCGCCGCCGC	CAGGCGGAGC
	CTCACACGAC	GGGCGCGACA	ACCTACGGCA	GGCGGCGGCG	GTCCGCCTCG
95	S V L	P A L L	D A V	R R R	Q A E L
351	TGAACCCGCG	CGCCCCGCGC	CTGCTGCGGA	GCCTGGAGGA	CGCAGCCCCG
	ACTTGGGCGC	GCGGGGCGCG	GACGACGCCT	CGGACCTCCT	GCGTCGGGCG
112	N P R	A P R	L L R S	L E D	A A R
401	CAGGTTCGGG	CCCTGGGCGC	CGCGGTGGAG	ACAGTGCTGG	CCGCGCTGGG
	GTCCAAGCCC	GGGACCCGCG	GCGCCACCTC	TGTCACGACC	GGCGCGACCC
128	Q V R A	L G A	A V E	T V L A	A L G
451	CGCTGCAGCC	CGCGGGCCCC	GGCCAGAGCC	CGTCACCGTC	GCCACCCTCT
	GCGACGTCGG	GCGCCCGGGC	CCGGTCTCGG	GCAGTGGCAG	CCGTGGGAGA
145	A A A	R G P G	P E P	V T V	A T L F
501	TCACGGCCAA	CAGCACTGCA	GGCATCTTCT	CAGCCAAGGT	GCTGGGGTTC
	AGTGCCGGTT	GTCGTGACGT	CCGTAGAAGA	GTCGGTTCCA	CGACCCCAAG
162	T A N	S T A	G I F S	A K V	L G F
551	CACGTGTGCG	GCCTCTATGG	CGAGTGGGTG	AGCCGCACAG	AGGGCGACCT
	GTGCACACGC	CGGAGATAACC	GCTCACCCAC	TCGGCGTGTC	TCCCGCTGGA
178	H V C G	L Y G	E W V	S R T E	G D L
601	GGGCCAGCTG	GTGCCAGGGG	GCGTCGCCTG	AGAGTGAATA	CTTTTTCTTG
	CCCGGTTCGAC	CACGGTCCCC	CGCAGCGGAC	TCTCACTTAT	GAAAAAGAAC
195	G Q L	V P G G	V A O		

FIG. 1B

651 TAAGCTCGCT CTGTCTCGCC TCTTTGGCTT CAAATTTTCT GTCTCTCCAT
ATTTCGAGCGA GACAGAGCGG AGAAACCGAA GTTTAAAAGA CAGAGAGGTA

701 CTGTGTCCTG TGTGTTCTTG GGCTGTCCCT ATCTTTCTGC ATTTGTGTGG
GACACAGGAC ACACAAGAAC CCGACAGGGA TAGAAAGACG TAAACACACC

751 TCTCTCTCTT CTGCTCTCCT CTCTGCAGGG AGCTTCTTTT TTCCAACAGT
AGAGAGAGAA GACGAGAGGA GAGACGTCCC TCGAAGAAAA AAGGTTGTCA

801 TTCTCGTTTT GTCTCTCTCC AGTCTTGAAC ACTTTTGTCT CCGAGAGGTC
AAGAGCAAAA CAGAGAGAGG TCAGAACTTG TGAAAACAGA GGCTCTCCAG

851 TCTTTTTTGT TCCTTGTCTC TTGGTTCTTT CTTTGCTTGC TTGCTTGCTT
AGAAAAACAA AGGAACAGAG AACCAAGAAA GAAACGAACG AACGAACGAA

901 GCTTGCTTGT TGTGAGACA GGGTCTCACC ATATAGCTCT GGATGGCCTG
CGAACGAACA ACAACTCTGT CCCAGAGTGG TATATCGAGA CCTACCGGAC

951 GAACTTGCTA TGTAGGCCAG GCTGGCCTCC AGCTCATAGA GATCCACTTG
CTTGAACGAT ACATCCGGTC CGACCGGAGG TCGAGTATCT CTAGGTGAAC

1001 CCTCCGACTC CCAATTTCCC CATCTGTCTC CCTGTGATCC ATATGGGTAT
GGAGGCTGAG GGTAAAGGG GTAGACAGAG GGACACTAGG TATACCCATA

1051 GTGTAACCCT TACTTTGTCT CATGGAGGTG ACAATTTTTC TCCCTTCAGT
CACATTGGGA ATGAAACAGA GTACCTCCAC TGTTAAAAAG AGGGAAGTCA

1101 TTCTTTGTTC TTTACTGACC AGAAAAGTGC CTA CTCTTGTCC CCTGGTGGCA
AAGAAACAAG AAATGACTGG TCTTTTCACG GATGAACAGG GGACCACCGT

1151 AGGCCATTCA CCTTAGGACC TTCCCACCAG TTCCTTTGTA GGCAAATCCC
TCCGGTAAGT GGAATCCTGG AAGGGTGGTC AAGGAAACAT CCGTTTAGGG

1201 TCCCCCTTTG AGGTCCTTCC CTTTCATACC GCCCTAGGCT GGTCAATGGA
AGGGGGAAAC TCCAGGAAGG GAAAGTATGG CGGGATCCGA CCAGTTACCT

1251 GAGAGAAAGG CAGAAAAACA TCTTTAAAGA GTTTTATTTG AGAATAAATT
CTCTCTTTCC GTCTTTTTGT AGAAATTTCT CAAAATAAAC TCTTATTTAA

1301 AATTTTTGTA AATAAAATGT TTAACAATAA AACTAAACTT TTATGAAAAA
TTAAAAACAT TTATTTTACA AATTGTTATT TTGATTTGAA AATACTTTTT

1351 AA (polyA)
TT

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FIG. 2

	10	20	30	40	50
chf.781	MSQREGSLEDHQTDSSISFLPHLEAKIRQTHNLARLLTKYAEQLLEEYVQ				
		**		***	* * *
humcntf	MAFTEHSPLTPHRRDLCSRSIWLARKIRSDLTALTESYVK				
		10	20	30	40

	60	70	80	90	100
chf.781	QQGEPFGLPGFSPRLPLAGLSGPAPSHAGLPVSERLRQDAAALSVLPAL				
	**	*	* *	***	* *
humcntf	HQGLNKNINLDSADGMPVA---STDQWSELTEAERLQENLQAYRTFHVL				
	50	60	70	80	

	110	120	130	140
chf.781	LD-AVRRRQAEELNPAPRLLRSLEDAARQVRALGAAVETVLAALGAAARG			
	*	*	* *	* *
humcntf	LARLLEDQQVHFTPTEGDFHQAIHTLLLQVAAFAYQIEELMILLEYKIPR			
	90	100	110	120

	150	160	170	180	190
chf.781	PGPEPVTVATLFTANSTAGIFSAKVLGFHVCGLYGEWVSRTEGDLGQLVP				
		* * *	* *	* *	**
humcntf	NEADGMPINV-----GDGGLFEKKLWGLKVLQELSQWTVRSIHDL-RFIS				
	140	150	160	170	180

	200
chf.781	GGVAO

humcntf	SHQTGIPARGSHYIANNKKM
	190 200

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FIG. 3

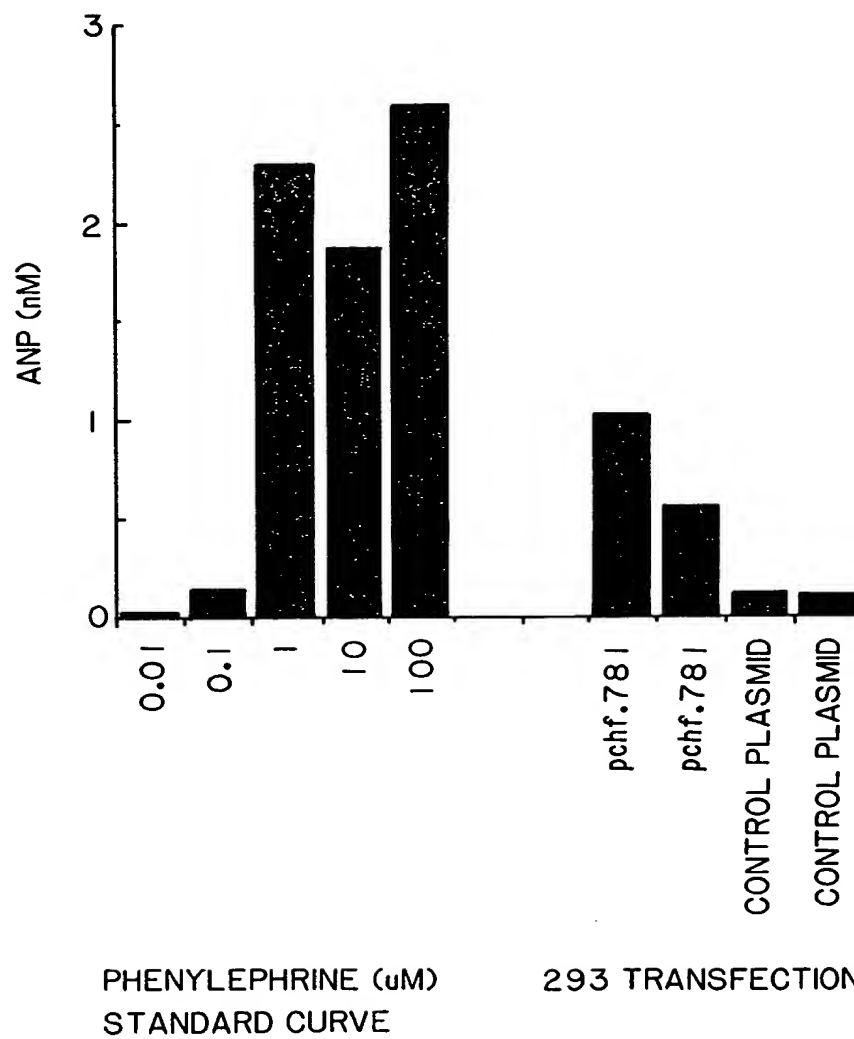
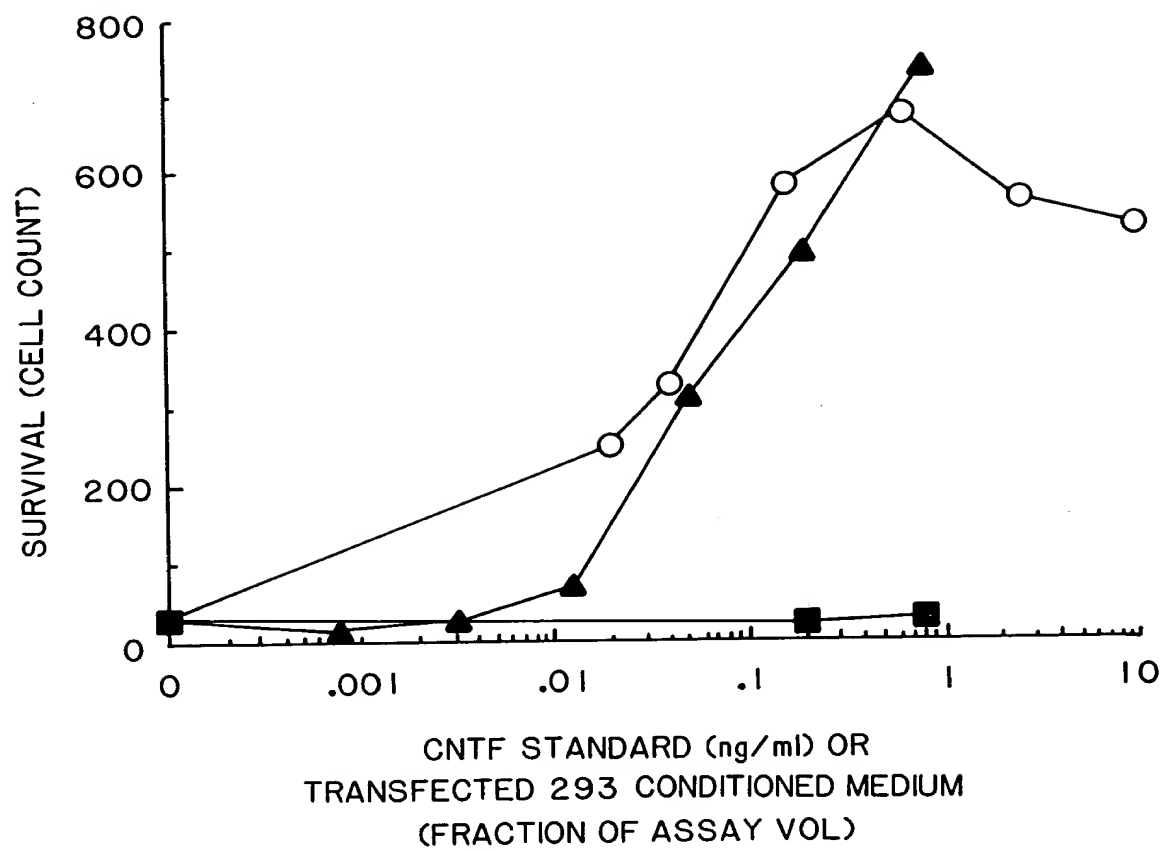


FIG. 4



[illegible]

1	GTGAAGGGAG	CCGGGATCAG	CCAGGGGCCA	GCATGAGCCG	GAGGGAGGGA
1	CACTTCCCTC	GGCCCTAGTC	GGTCCCCGGT	CGTACTCGGC	CTCCCTCCCT
				M S R	R E G
51	AGTCTGGAAG	ACCCCCAGAC	TGATTTCCTCA	GTCTCACTTC	TTCCCCACTT
7	TCAGACCTTC	TGGGGGTCTG	ACTAAGGAGT	CAGAGTGAAG	AAGGGGTGAA
	S L E D	P Q T	D S S	V S L L	P H L
101	GGAGGCCAAG	ATCCGTCAGA	CACACAGCCT	TGCGCACCTC	CTCACCAAAT
24	CCTCCGGTTC	TAGGCAGTCT	GTGTGTCTGGA	ACGCGTGGAG	GAGTGGTTTA
	E A K	I R Q T	H S L	A H L	L T K Y
151	ACGCTGAGCA	GCTGCTCCAG	GAATATGTGC	AGCTCCAGGG	AGACCCCTTC
41	TGCGACTCGT	CGACGAGGTC	CTTATACACG	TCGAGGTCCC	TCTGGGGAAG
	A E Q	L L Q	E Y V Q	L Q G	D P F
201	GGGCTGCCCA	GCTTCTCGCC	GCCGCGGCTG	CCGGTGGCCG	GCCTGAGCGC
57	CCCGACGGGT	CGAAGAGCGG	CGGCGCCGAC	GGCCACCGGC	CGGACTCGCG
	G L P S	F S P	P R L	P V A G	L S A
251	CCCGGCTCCG	AGCCACGCGG	GGCTGCCAGT	GCACGAGCGG	CTGCGGCTGG
74	GGGCCGAGGC	TCGGTGCGCC	CCGACGGTCA	CGTGCTCGCC	GACGCCGACC
	P A P	S H A G	L P V	H E R	L R L D
301	ACGCGGCGGC	GCTGGCCGCG	CTGCCCCCGC	TGCTGGACGC	AGTGTGTCGC
91	TGCGCCGCCG	CGACCGGCGC	GACGGGGGCG	ACGACCTGCG	TCACACAGCG
	A A A	L A A	L P P L	L D A	V C R
351	CGCCAGGCCG	AGCTGAACCC	GCGCGCGCCG	CGCCTGCTGC	GCCGCCTGGA
107	GCGGTCCGGC	TCGACTTGGG	CGCGCGCGGC	GCGGACGACG	CGGCGGACCT
	R Q A E	L N P	R A P	R L L R	R L E
401	GGACGCGGCG	CGCCAGGCCC	GGGCCCTGGG	CGCCGCCGTG	GAGGCCTTGC
124	CCTGCGCCGC	GCGGTCCGGG	CCCGGGACCC	GCGGCGGCAC	CTCCGGAACG
	D A A	R Q A R	A L G	A A V	E A L L
451	TGGCCGCGCT	GGGCGCCGCC	AACCGCGGGC	CCCGGGCCGA	GCCCCCGGCC
141	ACCGGCGCGA	CCCGCGGCGG	TTGGCGCCCC	GGGCCC GGCT	CGGGGGGCGG
	A A L	G A A	N R G P	R A E	P P A

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501	GCCACCGCCT	CAGCCGCCTC	CGCCACCGGG	GTCTTCCCCG	CCAAGGTGCT
	CGGTGGCGGA	GTCGGCGGAG	GCGGTGGCCC	CAGAAGGGGC	GGTTCCACGA
157	A T A S	A A S	A T G	V F P A	K V L
551	GGGGCTCCGC	GTTTGCGGCC	TCTACCGCGA	GTGGCTGAGC	CGCACCGAGG
	CCCCGAGGCG	CAAACGCCGG	AGATGGCGCT	CACCGACTCG	GCGTGGCTCC
174	G L R	V C G L	Y R E	W L S	R T E G
601	GCGACCTGGG	CCAGCTGCTG	CCCGGGGGCT	CGGCCTGAGC	GCCGCGGGGC
	CGTGGACCC	GGTCGACGAC	GGGCCCCCGA	GCCGGACTION	CGGCGCCCCG
191	D L G	Q L L	P G G S	A O	
651	AGCTCGCCCC	GCCTCCTCCC	GCTGGGTTC	GTCTCTCCTT	CCGCTTCTTT
	TCGAGCGGGG	CGGAGGAGGG	CGACCCAAGG	CAGAGAGGAA	GGCGAAGAAA
701	GTCTTTCTCT	GCCGCTGTCG	GTGTCTGTCT	GTCTGCTCTT	AGCTGTCTCC
	CAGAAAGAGA	CGGCGACAGC	CACAGACAGA	CAGACGAGAA	TCGACAGAGG
751	ATTGCCTCGG	CCTTCTTTGC	TTTTTGTGGG	GGAGAGGGGA	GGGGACGGGC
	TAACGGAGCC	GGAAGAAACG	AAAAACACCC	CCTCTCCCCT	CCCCTGCCCC
801	AGGGTCTCTG	TCGCCCAGGC	TGGGGTGCAG	TGGCGCGATC	CCAGCACTGC
	TCCCAGAGAC	AGCGGGTCCG	ACCCACGTC	ACCGCGCTAG	GGTCGTGACG
851	AGCCTCAACC	TCCTGGGCTC	AAGCCATCCT	TCCGCCTCAG	CTTCCCCAGC
	TCGGAGTTGG	AGGACCCGAG	TTCGGTAGGA	AGGCGGAGTC	GAAGGGGTGC
901	AGCTGGGACT	ACAGGCACGC	GCCACCACAG	CCGGCTAATT	TTTTATTTAA
	TCGACCCTGA	TGTCCGTGCG	CGGTGGTGTC	GGCCGATTAA	AAAATAAATT
951	TTTTTTGTAG	AGACGAGGTT	TCGCCATGTT	GCCCAGGCTG	GTCTTGAAC
	AAAAAACATC	TCTGCTCCAA	AGCGGTACAA	CGGGTCCGAC	CAGAACTTGA
1001	CCGGGGCTCA	AGCGATCC			
	GGCCCCGAGT	TCGCTAGG			

FIG. 6

humct1 1 MSRREGSLEDPQTDSSVSLLPHLEAKIRQTHSLAHLTKYAEQLLQEYVQLQG
 ** ***** **

chf.781 1 MSQREGSLEDHQTDSSISFLPHLEAKIRQTHNLARLLTKYAEQLLEEYVQQQG

humct1 54 DPFGLPSFSPRLPVAGLSAPAPSHAGLPVHERLRDAAALAALPPLLDVCR
 ***** **

chf.781 54 EPFGLPGFSPRLPLAGLSGPAPSHAGLPVSERLRQDAAALSVLPALLDAVRR

humct1 107 RQAE LNPRAPRLLRRLEDAARQARALGA AVEALLAALGAANRG PRAEPPAATA
 ***** **

chf.781 107 RQAE LNPRAPRLLRSLEDAARQVRALGA AVETVLAALGAAARGPGPEPVT VAT

humct1 160 --SAASATGVFPAKVLGLRVCGLYREWLSRTEGDLGQLLPGGSA
 * * * * *

chf.781 160 LFTANSTAGIFSAKVLGFHVCGLYGEWVSRTEGDLGQLVPGGVA

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